IN THE CLAIMS

Claim 1 is amended. Support for the amendment may be found e.g., in the original claim and on page 24, lines 11-13. Claim 6 is amended to correct a typographical error. No new matter is presented by the amendments.

CURRENT STATUS OF ALL CLAIMS IN THE APPLICATION

1. (currently and previously amended) A method for detecting a plurality of RNAs in a sample comprising:

hybridizing the sample with a substrate, wherein the substrate has a plurality of different probes and wherein the probes are suitable for multiple bases primer extension reactions;

synthesizing primer extension products with a nucleic acid polymerase, appropriate reagents and conditions, from the primers and using the RNAs as templates; and

detecting the primer extension products to determine the level of said plurality of RNAs.

2. (original) The method of Claim 1 wherein the nucleic acid polymerase is a reverse transcriptase.

3. (original) The method of Claim 2 wherein the reverse transcriptase is a thermostable reverse transcriptase.

4. (original) The method of Claim 2 wherein the probes are oligonucleotide probes.

5. (original) The method of Claim 4 wherein the oligonucleotide probes are immobilized on the substrate in 5'-3' direction.

6. (currently amended) The method of Claim 5 wherein the oligonucleotide probes are synthesized on the substrate~~d~~ in 5'-3' direction.

7. (original) The method of Claim 6 wherein the plurality of RNAs comprises at least 50 RNAs.

8. (original) The method of Claim 7 wherein the plurality of RNAs comprises at least 100 RNAs.

9. (original) The method of Claim 8 wherein the plurality of RNAs comprises at least 1000 RNAs.

10. (original) The method of Claim 9 wherein the plurality of RNAs comprises at least 5000 RNAs.

11. (original) The method of Claim 8 wherein each of the RNAs is targeted by at least 2 probes.

12. (original) The method of Claim 11 wherein each of the RNAs is targeted by at least 5 probes.

13. (original) The method of Claim 12 wherein each of the RNAs is targeted by at least 10 probes.

14. (original) The method of Claim 13 wherein each of the RNAs is targeted by at least 20 probes.

15. (original) The method of Claim 11 wherein the plurality of probes have at least 100 probes per cm^2 of the substrate.

16. (original) The method of Claim 15 wherein the plurality of probes have at least 1000 probes per cm^2 of the substrate.

17. (original) The method of Claim 16 wherein the plurality of probes have at least 10000 probes per cm^2 of the substrate

18. (original) The method of Claim 11 wherein the extension products are detected by using a label.

19. (original) The method of Claim 18 wherein the label is incorporated during the synthesizing.

20. (previously amended) The method of Claim 18 wherein the label is attached to the extension products after the synthesizing of primer extension products with a nucleic acid polymenrase.

21. (original) The method of Claim 19 wherein the reagent comprises at least one type of ddNTP.

22. (original) The method of Claim 21 wherein at least one type of ddNTP is labeled.

23. (original) The method of Claim 22 wherein the ddNTP is labeled with a biotin.

24. (original) The method of Claim 22 wherein the reagent comprises at least one type of dNTP.

25. (original) The method of Claim 24 wherein the reagent comprises dATP, dCTP, dGTP, and dTTP.

26. (original) The method of Claim 11 wherein the probes comprise tiling probes that are selected to tile regions of the RNA, and the method of Claim 11 further comprising determining sequence variations by detecting the extension products of the tiling probes.

27. (original) The method of Claim 26 wherein the sequence variations are SNPs.

28. (original) The method of Claim 11 wherein the probes comprise tiling probes that are selected to tile the bordering regions of exons or putative exons, and the method of Claim 11 further comprising determining the arrangement of exons in the RNAs by detecting the extension products of the tiling probes.

29. (original) The method of Claim 11 wherein the probes comprises probes that are designed to target subregions of a genomic sequence and the method of Claim 11 further comprises determining whether the subregions of the genomic sequence is transcribed by detecting the extension products of the probes designed to target the subregions of the genomic sequence.